

0210

OIPE

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RAW SEQUENCE LISTING                      DATE: 07/05/2000  
 PATENT APPLICATION:    US/09/598,982        TIME: 18:43:07

Input Set : A:\Tryptase.app  
 Output Set: N:\CRF3\07052000\I598982.raw

ENTERED

3 <110> APPLICANT: NILES, ANDREW L  
 4        MAFFITT, MARK A  
 5        HAAK-FRENDSCHO, MARY  
 7 <120> TITLE OF INVENTION: RECOMBINANT PROTEOLYTIC TYPTASES, ACTIVE SITE MUTANTS  
 8        THEREOF, AND METHODS OF MAKING SAME  
 10 <130> FILE REFERENCE: CIP TRYPTASE  
 12 <140> CURRENT APPLICATION NUMBER: US/09/598,982  
 C--> 13 <141> CURRENT FILING DATE: 2000-06-21  
 15 <150> PRIOR APPLICATION NUMBER: 09/079,970  
 16 <151> PRIOR FILING DATE: 1998-04-15  
 18 <160> NUMBER OF SEQ ID NOS: 51  
 20 <170> SOFTWARE: PatentIn Ver. 2.0  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 735  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo sapiens  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (1)..(735)  
 31 <400> SEQUENCE: 1  
 32 atc gtc ggg ggt cag gag gcc ccc agg agc aag tgg ccc tgg cag gtg    48  
 33 Ile Val Gly Gly Gln Glu Ala Pro Arg Ser Lys Trp Pro Trp Gln Val  
 34    1                      5                      10                      15  
 36 agc ctg aga gtc cac ggc cca tac tgg atg cac ttc tgc ggg ggc tcc    96  
 37 Ser Leu Arg Val His Gly Pro Tyr Trp Met His Phe Cys Gly Gly Ser  
 38                      20                      25                      30  
 40 ctc atc cac ccc cag tgg gtg ctg acc gca gcg cac tgc gtg gga ccg    144  
 41 Leu Ile His Pro Gln Trp Val Leu Thr Ala Ala His Cys Val Gly Pro  
 42                      35                      40                      45  
 44 gac gtc aag gat ctg gcc gcc ctc agg gtg caa ctg cgg gag cag cac    192  
 45 Asp Val Lys Asp Leu Ala Ala Leu Arg Val Gln Leu Arg Glu Gln His  
 46                      50                      55                      60  
 48 ctc tac tac cag gac cag ctg ctg ccg gtc agc agg atc atc gtg cac    240  
 49 Leu Tyr Tyr Gln Asp Gln Leu Leu Pro Val Ser Arg Ile Ile Val His  
 50    65                      70                      75                      80  
 52 cca cag ttc tac acc gcc cag atc gga gcg gac atc gcc ctg ctg gag    288  
 53 Pro Gln Phe Tyr Thr Ala Gln Ile Gly Ala Asp Ile Ala Leu Leu Glu  
 54                      85                      90                      95  
 56 ctg gag gag ccg gtg aac gtc tcc agc cac gtc cac acg gtc acc ctg    336  
 57 Leu Glu Glu Pro Val Asn Val Ser Ser His Val His Thr Val Thr Leu  
 58                      100                      105                      110  
 60 ccc cct gcc tca gag acc ttc ccc ccg ggg atg ccg tgc tgg gtc act    384  
 61 Pro Pro Ala Ser Glu Thr Phe Pro Pro Gly Met Pro Cys Trp Val Thr  
 62                      115                      120                      125  
 64 ggc tgg ggc gat gtg gac aat gat gag cgc ctc cca ccg cca ttt cct    432  
 65 Gly Trp Gly Asp Val Asp Asn Asp Glu Arg Leu Pro Pro Pro Phe Pro  
 66    130                      135                      140

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68 ctg aag cag gtg aag gtc ccc ata atg gaa aac cac att tgt gac gca 480
69 Leu Lys Gln Val Lys Val Pro Ile Met Glu Asn His Ile Cys Asp Ala
70 145 150 155 160
72 aaa tac cac ctt ggc gcc tac acg gga gac gac gtc cgc atc gtc cgt 528
73 Lys Tyr His Leu Gly Ala Tyr Thr Gly Asp Asp Val Arg Ile Val Arg
74 165 170 175
76 gac gac atg ctg tgt gcc ggg aac acc cgg agg gac tca tgc cag ggc 576
77 Asp Asp Met Leu Cys Ala Gly Asn Thr Arg Arg Asp Ser Cys Gln Gly
78 180 185 190
80 gac tcc gga ggg ccc ctg gtg tgc aag gtg aat ggc acc tgg ctg cag 624
81 Asp Ser Gly Gly Pro Leu Val Cys Lys Val Asn Gly Thr Trp Leu Gln
82 195 200 205
84 ggc ggc gtg gtc agc tgg ggc gag ggc tgt gcc cag ccc aac cgg cct 672
85 Ala Gly Val Val Ser Trp Gly Glu Gly Cys Ala Gln Pro Asn Arg Pro
86 210 215 220
88 ggc atc tac acc cgt gtc acc tac tac ttg gac tgg atc cac cac tat 720
89 Gly Ile Tyr Thr Arg Val Thr Tyr Tyr Leu Asp Trp Ile His His Tyr
90 225 230 235 240
92 gtc ccc aaa aag ccg 735
93 Val Pro Lys Lys Pro
94 245
97 <210> SEQ ID NO: 2
98 <211> LENGTH: 245
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 2
103 Ile Val Gly Gly Gln Glu Ala Pro Arg Ser Lys Trp Pro Trp Gln Val
104 1 5 10 15
106 Ser Leu Arg Val His Gly Pro Tyr Trp Met His Phe Cys Gly Gly Ser
107 20 25 30
109 Leu Ile His Pro Gln Trp Val Leu Thr Ala Ala His Cys Val Gly Pro
110 35 40 45
112 Asp Val Lys Asp Leu Ala Ala Leu Arg Val Gln Leu Arg Glu Gln His
113 50 55 60
115 Leu Tyr Tyr Gln Asp Gln Leu Leu Pro Val Ser Arg Ile Ile Val His
116 65 70 75 80
118 Pro Gln Phe Tyr Thr Ala Gln Ile Gly Ala Asp Ile Ala Leu Leu Glu
119 85 90 95
121 Leu Glu Glu Pro Val Asn Val Ser Ser His Val His Thr Val Thr Leu
122 100 105 110
124 Pro Pro Ala Ser Glu Thr Phe Pro Pro Gly Met Pro Cys Trp Val Thr
125 115 120 125
127 Gly Trp Gly Asp Val Asp Asn Asp Glu Arg Leu Pro Pro Pro Phe Pro
128 130 135 140
130 Leu Lys Gln Val Lys Val Pro Ile Met Glu Asn His Ile Cys Asp Ala
131 145 150 155 160
133 Lys Tyr His Leu Gly Ala Tyr Thr Gly Asp Asp Val Arg Ile Val Arg
134 165 170 175
136 Asp Asp Met Leu Cys Ala Gly Asn Thr Arg Arg Asp Ser Cys Gln Gly

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/598,982  
 DATE: 07/05/2000  
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Input Set : A:\Tryptase.app  
 Output Set: N:\CRF3\07052000\I598982.raw

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137                               180                               185                               190
139 Asp Ser Gly Gly Pro Leu Val Cys Lys Val Asn Gly Thr Trp Leu Gln
140                               195                               200                               205
142 Ala Gly Val Val Ser Trp Gly Glu Gly Cys Ala Gln Pro Asn Arg Pro
143                               210                               215                               220
145 Gly Ile Tyr Thr Arg Val Thr Tyr Tyr Leu Asp Trp Ile His His Tyr
146 225                               230                               235                               240
148 Val Pro Lys Lys Pro
149                               245
152 <210> SEQ ID NO: 3
153 <211> LENGTH: 40
154 <212> TYPE: DNA
155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR Primer
160 <400> SEQUENCE: 3
161 gggcccctcg agaaaagaat cgtcgggggt caggaggccc 40
164 <210> SEQ ID NO: 4
165 <211> LENGTH: 40
166 <212> TYPE: DNA
167 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
170 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR Primer
172 <400> SEQUENCE: 4
173 ccactatgtc cccaaaaagc cgtgaagcgg ccgccgtcgt 40
176 <210> SEQ ID NO: 5
177 <211> LENGTH: 771
178 <212> TYPE: DNA
179 <213> ORGANISM: Homo sapiens
181 <220> FEATURE:
182 <221> NAME/KEY: CDS
183 <222> LOCATION: (7)..(753)
185 <400> SEQUENCE: 5
186 gggccc ctc gag aaa aga atc gtc ggg ggt cag gag gcc ccc agg agc 48
187 Leu Glu Lys Arg Ile Val Gly Gly Gln Glu Ala Pro Arg Ser
188 1 5 10
190 aag tgg ccc tgg cag gtg agc ctg aga gtc cac ggc cca tac tgg atg 96
191 Lys Trp Pro Trp Gln Val Ser Leu Arg Val His Gly Pro Tyr Trp Met
192 15 20 25 30
194 cac ttc tgc ggg ggc tcc ctc atc cac ccc cag tgg gtg ctg acc gca 144
195 His Phe Cys Gly Gly Ser Leu Ile His Pro Gln Trp Val Leu Thr Ala
196 35 40 45
198 gcg cac tgc gtg gga ccg gac gtc aag gat ctg gcc gcc ctc agg gtg 192
199 Ala His Cys Val Gly Pro Asp Val Lys Asp Leu Ala Ala Leu Arg Val
200 50 55 60
202 caa ctg cgg gag cag cac ctc tac tac cag gac cag ctg ctg ccg gtc 240
203 Gln Leu Arg Glu Gln His Leu Tyr Tyr Gln Asp Gln Leu Leu Pro Val
204 65 70 75
206 agc agg atc atc gtg cac cca cag ttc tac acc gcc cag atc gga gcg 288

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207 Ser Arg Ile Ile Val His Pro Gln Phe Tyr Thr Ala Gln Ile Gly Ala
208      80      85      90
210 gac atc gcc ctg ctg gag ctg gag gag ccg gtg aac gtc tcc agc cac 336
211 Asp Ile Ala Leu Leu Glu Leu Glu Glu Pro Val Asn Val Ser Ser His
212 95      100      105      110
214 gtc cac acg gtc acc ctg ccc cct gcc tca gag acc ttc ccc ccg ggg 384
215 Val His Thr Val Thr Leu Pro Pro Ala Ser Glu Thr Phe Pro Pro Gly
216      115      120      125
218 atg ccg tgc tgg ctg act ggc tgg ggc gat gtg gac aat gat gag cgc 432
219 Met Pro Cys Trp Val Thr Gly Trp Gly Asp Val Asp Asn Asp Glu Arg
220      130      135      140
222 ctc cca ccg cca ttt cct ctg aag cag gtg aag gtc ccc ata atg gaa 480
223 Leu Pro Pro Pro Phe Pro Leu Lys Gln Val Lys Val Pro Ile Met Glu
224      145      150      155
226 aac cac att tgt gac gca aaa tac cac ctt ggc gcc tac acg gga gac 528
227 Asn His Ile Cys Asp Ala Lys Tyr His Leu Gly Ala Tyr Thr Gly Asp
228 160      165      170
230 gac gtc cgc atc gtc cgt gac gac atg ctg tgt gcc ggg aac acc cgg 576
231 Asp Val Arg Ile Val Arg Asp Asp Met Leu Cys Ala Gly Asn Thr Arg
232 175      180      185      190
234 agg gac tca tgc cag ggc gac tcc gga ggg ccc ctg gtg tgc aag gtg 624
235 Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Val
236      195      200      205
238 aat ggc acc tgg ctg cag ggc ggc gtg gtc agc tgg ggc gag ggc tgt 672
239 Asn Gly Thr Trp Leu Gln Ala Gly Val Val Ser Trp Gly Glu Gly Cys
240      210      215      220
242 gcc cag ccc aac cgg cct ggc atc tac acc cgt gtc acc tac tac ttg 720
243 Ala Gln Pro Asn Arg Pro Gly Ile Tyr Thr Arg Val Thr Tyr Tyr Leu
244      225      230      235
246 gac tgg atc cac cac tat gtc ccc aaa aag ccg tgaagcggcc gccgtcgt 771
247 Asp Trp Ile His His Tyr Val Pro Lys Lys Pro
248      240      245
251 <210> SEQ ID NO: 6
252 <211> LENGTH: 249
253 <212> TYPE: PRT
254 <213> ORGANISM: Homo sapiens
256 <400> SEQUENCE: 6
257 Leu Glu Lys Arg Ile Val Gly Gly Gln Glu Ala Pro Arg Ser Lys Trp
258 1      5      10      15
260 Pro Trp Gln Val Ser Leu Arg Val His Gly Pro Tyr Trp Met His Phe
261      20      25      30
263 Cys Gly Gly Ser Leu Ile His Pro Gln Trp Val Leu Thr Ala Ala His
264      35      40      45
266 Cys Val Gly Pro Asp Val Lys Asp Leu Ala Ala Leu Arg Val Gln Leu
267      50      55      60
269 Arg Glu Gln His Leu Tyr Tyr Gln Asp Gln Leu Leu Pro Val Ser Arg
270      65      70      75      80
272 Ile Ile Val His Pro Gln Phe Tyr Thr Ala Gln Ile Gly Ala Asp Ile
273      85      90      95

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275 Ala Leu Leu Glu Leu Glu Glu Pro Val Asn Val Ser Ser His Val His
276      100      105      110
278 Thr Val Thr Leu Pro Pro Ala Ser Glu Thr Phe Pro Pro Gly Met Pro
279      115      120      125
281 Cys Trp Val Thr Gly Trp Gly Asp Val Asp Asn Asp Glu Arg Leu Pro
282      130      135      140
284 Pro Pro Phe Pro Leu Lys Gln Val Lys Val Pro Ile Met Glu Asn His
285 145      150      155      160
287 Ile Cys Asp Ala Lys Tyr His Leu Gly Ala Tyr Thr Gly Asp Asp Val
288      165      170      175
290 Arg Ile Val Arg Asp Asp Met Leu Cys Ala Gly Asn Thr Arg Arg Asp
291      180      185      190
293 Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Val Asn Gly
294      195      200      205
296 Thr Trp Leu Gln Ala Gly Val Val Ser Trp Gly Glu Gly Cys Ala Gln
297      210      215      220
299 Pro Asn Arg Pro Gly Ile Tyr Thr Arg Val Thr Tyr Tyr Leu Asp Trp
300 225      230      235      240
302 Ile His His Tyr Val Pro Lys Lys Pro
303      245
306 <210> SEQ ID NO: 7
307 <211> LENGTH: 27
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: Description of Artificial Sequence: Mutagenesis
313      Oligo
315 <400> SEQUENCE: 7
316 gaggagcccg tgaaggtctc cagccac      27
319 <210> SEQ ID NO: 8
320 <211> LENGTH: 771
321 <212> TYPE: DNA
322 <213> ORGANISM: Homo sapiens
324 <220> FEATURE:
325 <221> NAME/KEY: CDS
326 <222> LOCATION: (7)..(753)
328 <400> SEQUENCE: 8
329 gggccc ctc gag aaa aga atc gtc ggg ggt cag gag gcc ccc agg agc      48
330      Leu Glu Lys Arg Ile Val Gly Gly Gln Glu Ala Pro Arg Ser
331      1      5      10
333 aag tgg ccc tgg cag gtg agc ctg aga gtc cac ggc cca tac tgg atg      96
334 Lys Trp Pro Trp Gln Val Ser Leu Arg Val His Gly Pro Tyr Trp Met
335 15      20      25      30
337 cac ttc tgc ggg ggc tcc ctc atc cac ccc cag tgg gtg ctg acc gca      144
338 His Phe Cys Gly Gly Ser Leu Ile His Pro Gln Trp Val Leu Thr Ala
339      35      40      45
341 gcg cac tgc gtg gga ccg gac gtc aag gat ctg gcc gcc ctc agg gtg      192
342 Ala His Cys Val Gly Pro Asp Val Lys Asp Leu Ala Ala Leu Arg Val
343      50      55      60

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VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/598,982

DATE: 07/05/2000  
TIME: 18:43:08

Input Set : A:\Tryptase.app  
Output Set: N:\CRF3\07052000\I598982.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date